

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 12:16:30 ; Search time 15.16 Seconds
(without alignments)
31.692 Million cell updates/sec

Title: US-09-759-484-3

Perfect score: 22

Sequence: 1 AMVSE 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	64	2	AN2538
2	22	100.0	130	2	S36103
3	22	100.0	171	2	S09385
4	22	100.0	202	2	S68609
5	22	100.0	214	2	T22896
6	22	100.0	215	2	T22895
7	22	100.0	238	2	C63240
8	22	100.0	246	2	AF1057
9	22	100.0	343	1	A44118
10	22	100.0	345	2	H90366
11	22	100.0	346	1	LJHU
12	22	100.0	346	1	S28228
13	22	100.0	346	1	LJRT1
14	22	100.0	346	1	LJRT1
15	22	100.0	346	2	LJRT1
16	22	100.0	379	2	S29978
17	22	100.0	395	2	T15302
18	22	100.0	398	2	E5306
19	22	100.0	406	1	T34839
20	22	100.0	454	2	G95047
21	22	100.0	454	2	F97918
22	22	100.0	474	2	T27006
23	22	100.0	496	2	C87638
24	22	100.0	523	1	TVEFMT
25	22	100.0	530	2	D82412
26	22	100.0	533	2	B84550
27	22	100.0	787	2	F97188
28	22	100.0	1056	2	B82557
29	22	100.0	1345	2	T00964

ALIGNMENTS

30	21	95.5	148	2	A75193	probable transcrip
31	21	95.5	200	2	E71495	probable n-acetyl
32	21	95.5	208	2	E71524	hypothetical prote
33	21	95.5	279	1	I64009	hypothetical prote
34	21	95.5	328	2	E83831	hypothetical prote
35	21	95.5	333	2	I40791	acetoaldehyde dehydrogen
36	21	95.5	344	2	C84015	transcription regu
37	21	95.5	360	2	H83650	hypothetical prote
38	21	95.5	398	2	F83999	hypothetical prote
39	21	95.5	458	1	S74543	nicotinate phospho
40	21	95.5	504	2	E95276	transcription term
41	21	95.5	519	2	S33661	probable aldehyde
42	21	95.5	543	2	S70013	rpx protein - Bac
43	21	95.5	553	1	S29861	chaperonin-like pr
44	21	95.5	576	2	B86499	hybrid cluster [4F
45	21	95.5	576	2	B72125	CT288 hypothetical

RESULT 1
AN2538
hypothetical protein asr7595 [imported] - Anabaena sp. (strain PCC 7120) plasmid pcc7
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AN2538
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AN2538
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-64 <KUR>
A:Cross-references: GB:AP003602; PIDN:BAW7238.1; PID:g17134680; GSPDB:GN00181
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: asr7595
A:Genome: plasmid

Query Match 100.0%; Score 22; DB 2; Length 64;
Best local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMVSE 5
DB 33 AMVSE 37

RESULT 2
S36103
annexin I - chicken (fragment)
N:Alternate names: lipocortin I
C:Species: Gallus gallus (chicken)
C:Date: 10-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
C:Accession: S36103
R:Stidls, Y.; Horseman, N.D.
FEBS Lett. 329, 296-300, 1993
A:Title: The hinge region of chicken annexin I contains no site for tyrosine phosphor
A:Reference number: S36103; MUID:93374034
A:Accession: S36103
A:Molecule type: mRNA
A:Residues: 1-130 <SID>
A:Cross-references: EMBL:S64951; NID:g408871; PIDN:AAB28036.1; PID:g408872
A:Note: the authors translated in fig. 3 the codon CTG for residues 8, 87 and 95 as T
C:Genetics:
A:Gene: anxi
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: calcium binding; phospholipid binding

F:40-111/Domain: annexin repeat homology <AX1>

Query Match 100.0%; Score 22; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
| | | | |
Db 2 AMVSE 6

RESULT 3

S09385
DNA-Invertase homolog bin3 - Staphylococcus aureus transposon Tn555

C:Species: Staphylococcus aureus
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Aug-1998
C:Accession: S09385

R:Rowland, S.J.; Dyke, K.G.H.

EMBO J. 8, 2761-2773, 1989

A:Title: Characterization of the staphylococcal beta-lactamase transposon Tn552.

A:Reference number: S09385; MUID:90060039

A:Accession: S09385

A:Molecule type: DNA

A:Residues: 1-171 <ROM>

A:Cross-references: EMBL:X16298

C:Genetics:

A:Gene: bin3

A:Mobile element: transposon Tn555

C:Superfamily: transposase repressor

C:Keywords: DNA binding

Query Match 100.0%; Score 22; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
| | | | |
Db 118 AMVSE 122

RESULT 4

S68609
recombinase Sin - Staphylococcus aureus plasmid pSKI

C:Species: Staphylococcus aureus
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C:Accession: S68609

R:Paulsen, I.T.; Gillespie, M.T.; Littlejohn, T.G.; Hanvivatvong, O.; Rowland, S.J.; Dyk

Gene 141, 109-114, 1994

A:Title: Characterisation of sin, a potential recombinase-encoding gene from Staphylococ

A:Reference number: S68609; MUID:94215871

A:Accession: S68609

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-202 <PAU>

A:Cross-references: EMBL:L23109; NID:9495088; PIDN:AAA26675.1; PID:9495089

C:Genetics:

A:Genome: plasmid

C:Superfamily: transposase repressor

Query Match 100.0%; Score 22; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
| | | | |
Db 118 AMVSE 122

RESULT 5

T22896

hypothetical protein F58B3.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000

C:Accession: T22896

R:Harris, B.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z19633

A:Accession: T22896

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-214 <WIL>

A:Cross-references: EMBL:Z73427; PIDN:CAA97801.1; GSPDB:GNO0022; CESP:F58B3.3

A:Experimental source: clone F58B3

C:Genetics:

A:Gene: CESP:F58B3.3

A:Map position: 4

A:Insertions: 68/1

C:Superfamily: Caenorhabditis elegans hypothetical protein F58B3.3

Query Match 100.0%; Score 22; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
| | | | |
Db 131 AMVSE 135

RESULT 6

T22895
hypothetical protein F58B3.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T22895

R:Harris, B.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z19633

A:Accession: T22895

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-215 <WIL>

A:Cross-references: EMBL:Z73427; PIDN:CAA97800.1; GSPDB:GNO0022; CESP:F58B3.2

A:Experimental source: clone F58B3

C:Genetics:

A:Gene: CESP:F58B3.2

A:Map position: 4

A:Insertions: 69/1

C:Superfamily: Caenorhabditis elegans hypothetical protein F58B3.3

Query Match 100.0%; Score 22; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
| | | | |
Db 132 AMVSE 136

RESULT 7

C83240
probable transcription regulator PA3249 [Imported] - Pseudomonas aeruginosa (strain P

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: C83240

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; L

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A62950; MUID:20437337

A:Accession: C83240

A;Reference number: A
A;Accession: A38909
A;Molecule type: mRNA

annexin I - human

N:Alternate names: calpactin II; lipocortin I; p35; phospholipase A2 inhibitory protein
 C:Species: Homo sapiens (man)
 C>Date: 04-Dec-1986 #sequence, revision 30-Sep-1992 #text_change 22-Jun-1999
 C:Accession: A03080; A28641; A38842; A34459; S07909; S28846
 R:Mailner, B.P.; Mattaliano, R.J.; Hession, C.; Cate, R.L.; Tizard, R.; Sinclair, L.K.;
 Nature 320, 77-81, 1986
 A:Title: Cloning and expression of human lipocortin, a phospholipase A2 inhibitor with F
 A:Reference number: A03080; MUID:86146879
 A:Accession: A03080
 A:Molecule type: mRNA
 A:Residues: 1-346 <NAL>
 A:Cross-references: EMBL:X05908; NID:934387; PIDN:CAA29338.1; PID:934388
 R:Varticovski, L.; Chahwala, S.B.; Whitman, M.; Cantley, L.; Schindler, D.; Chow, E.P.;
 Biochemistry 27, 3682-3690, 1988
 A:Title: Location of sites in human lipocortin I that are phosphorylated by protein tyro
 A:Reference number: A28641; MUID:88309771
 A:Accession: A28641
 A:Molecule type: protein
 A:Residues: 10-26;214-233 <VAR>
 R:Peplinsky, R.B.; Sinclair, L.K.; Chow, E.P.; O'Brien-Greco, B.
 Biochem. J. 263, 97-103, 1989
 A:Title: A dimeric form of lipocortin-1 in human placenta.
 A:Reference number: A38842; MUID:90104259
 A:Accession: A38842
 A:Molecule type: protein
 A:Residues: 10-18, 'X', 20-26;30-49;59-71;129-144;215-228;318-323, 'X', 325-332 <PEP>
 A:Experimental source: placenta
 A:Note: in placenta, approximately 20% of annexin I was observed as a dimer; the authors
 R:Kovacic, R.T.; Tizard, R.; Cate, R.L.; Frey, A.Z.; Mailner, B.P.
 Biochem. J. 30, 9015-9021, 1991
 A:Title: Correlation of gene and protein structure of rat and human lipocortin I.
 A:Reference number: A40301; MUID:91369906
 A:Accession: A40301
 A:Contents: annotation
 R:Blummann, K.; Scoble, H.A.
 Science 233, 992-998, 1987
 A:Title: Characterization by tandem mass spectrometry of structural modifications in pro
 A:Reference number: A38843; MUID:87292145
 A:Contents: annotation; amino-terminal acetylation
 R:Arcone, R.; Alpala, G.; Ruppolo, M.; Malorni, A.; Pucci, P.; Marino, G.; Talenti, A.;
 Eur. J. Biochem. 211, 347-352, 1993
 A:Title: Structural characterization of a biologically active human lipocortin I express
 A:Reference number: S28846; MUID:93145967
 A:Accession: S28846
 A:Contents: annotation
 R:Hayashi, H.; Owada, M.K.; Sonobe, S.; Kakunaga, T.
 J. Biol. Chem. 264, 17222-17230, 1989
 A:Title: Characterizations of two distinct Ca(2+)-dependent phospholipid-binding protein
 A:Reference number: A34459; MUID:90008880
 A:Accession: A34459
 A:Molecule type: protein
 A:Residues: 30-45;82-97;114-128;148-161;275-281 <HAV>
 C:Comment: Annexin undergo reversible, calcium-dependent binding to membrane phospholip
 derstool.
 C:Comment: Annexin I has been shown to be both an intracellular and an extracellular pro
 ctivity. Unphosphorylated it is a potent inhibitor of the enzyme, mimicking the ameliore
 pids. Phosphorylation of annexin I results in loss of its inhibitory activity.
 C:Comment: This protein contains four homologous repeats. Each contains an "endoneixin fo
 and phospholipid.
 C:Genetics: GDB:ANX1
 A:Gene: GDB:ANX1
 A:Cross-references: GDB:120550; OMIM:151690
 A:Map position: 9q11-9q22
 A:Introns: 22/3; 59/1; 90/3; 128/3; 159/1; 185/3; 204/3; 236/1; 268/1; 287/3; 328/3
 C:Superfamily: annexin I; annexin repeat homology
 C:Keywords: acetylated amino end; calcium binding; duplication; endoneixin fold; glycopro
 F:2-346/Product: annexin I #status predicted <MAT>
 F:45-116/Domian: annexin repeat homology <AX1>
 F:56-72/Region: endoneixin fold #status predicted
 F:117-188/Domian: annexin repeat homology <AX2>
 F:128-144/Region: endoneixin fold #status predicted
 F:200-272/Domian: annexin repeat homology <AX3>
 F:212-228/Region: endoneixin fold #status predicted
 F:276-346/Domian: annexin repeat homology <AX4>
 F:287-303/Region: endoneixin fold #status predicted

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
 F:21/Binding site: phosphate (Tyr) (covalent) (by EGF receptor/kinase) #status experi
 F:27/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experimen
 F:43/Binding site: carboxylate (Asn) (covalent) #status absent
 F:216/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status exp

Query Match 100.0%; Score 22; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
 |||||
 Db 2 AMVSE 6

RESULT 12

S28228
 N:Alternate names: calpactin II
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 13-Jan-1995 #sequence, revision 05-Apr-1995 #text_change 22-Jun-1999
 C:Accession: S28228; A60851
 R:Ernst, J.D.
 Biochem. J. 289, 539-542, 1993
 A:Title: Epitope mapping of annexin I: antibodies that compete with phospholipids and
 A:Reference number: S28228; MUID:91143727
 A:Accession: S28228
 A:Molecule type: nucleic acid sequence not shown
 A>Status: nucleic acid sequence not shown
 A:Residues: 1-346 <ERN>
 A:Cross-references: EMBL:X56649; NID:973; PIDN:CAA39971.1; PID:974
 A:Experimental source: Madin-Darby kidney cell line
 R:Glennay Jr., J.R.; Tack, B.; Powell, M.A.
 J. Cell Biol. 104, 503-511, 1987
 A:Title: Calpactins: two distinct Ca(++)-regulated phospholipid- and actin-binding pr
 A:Reference number: A60851; MUID:87137890
 A:Accession: A60851
 A:Molecule type: protein
 A:Residues: 13-40 <GLE>
 A:Experimental source: lung
 A:Comment: Annexin undergo reversible, calcium-dependent binding to membrane phospho
 derstool.
 C:Comment: Annexin I has been shown to be both an intracellular and an extracellular
 ctivity. Unphosphorylated it is a potent inhibitor of the enzyme, mimicking the ameli
 pids. Phosphorylation of annexin I results in loss of its inhibitory activity.
 C:Comment: This protein contains four homologous repeats. Each contains an "endoneixin
 and phospholipid.
 C:Superfamily: annexin I; annexin repeat homology
 C:Keywords: blocked amino end; calcium binding; duplication; endoneixin fold; glycopro
 F:2-346/Product: annexin I #status predicted <MAT>
 F:45-116/Domian: annexin repeat homology <AX1>
 F:56-72/Region: endoneixin fold #status predicted
 F:117-188/Domian: annexin repeat homology <AX2>
 F:128-144/Region: endoneixin fold #status predicted
 F:200-272/Domian: annexin repeat homology <AX3>
 F:212-228/Region: endoneixin repeat homology <AX4>
 F:276-346/Domian: annexin repeat homology <AX5>
 F:287-303/Region: endoneixin fold #status predicted
 F:216/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #st
 F:21/Binding site: phosphate (Tyr) (covalent) (by EGF receptor/kinase) #status predic
 F:216/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pre

Query Match 100.0%; Score 22; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
 |||||
 Db 2 AMVSE 6

RESULT 13

LUTR1

annexin I - rat

N:Alternate names: calpactin II; lipocortin I; p35; phospholipase A2 inhibitory protein

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text_change 22-Jun-1999

C:Accession: J0303; A26841; A40301; A30896; B53507

R:Shimizu, Y.; Takabayashi, E.; Yano, S.; Shimizu, N.; Yamada, K.; Gushima, H.

Gene 65, 141-147, 1988

A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rat

A:Reference number: A91595; MUID:88284376

A:Accession: J0303

A:Molecule type: mRNA

A:Residues: 1-346 <SHI>

A:Cross-references: GB:M9967; NID:9203251; PIDN:AAA0861.1; PID:9203252

R:Tamaki, M.; Nakamura, E.; Nishikubo, C.; Sakata, T.; Shin, M.; Teraoka, H.

Nucleic Acids Res. 15, 7637, 1987

A:Title: Rat lipocortin I cDNA.

A:Reference number: A26841; MUID:88015620

A:Accession: A26841

A:Molecule type: mRNA

A:Residues: 1-346 <TAM>

A:Cross-references: GB:Y00446; NID:956565; PIDN:CAA68500.1; PID:956566

R:Kowalczyk, R.T.; Tizard, R.; Gate, R.L.; Frey, A.Z.; Wallner, B.F.

Biochemistry 30, 9015-9021, 1991

A:Title: Correlation of gene and protein structure of rat and human lipocortin I.

A:Reference number: A40301; MUID:91369906

A:Accession: A40301

A:Molecule type: DNA

A:Residues: 1-321, 'S', 323-346 <KOV>

A:Cross-references: GB:S57478; GB:005339; NID:9235878; PIDN:AA19866.1; PID:9235879

R:Pejlsnik, R.B.; Sinclair, L.K.; Browning, J.L.; Mattaliano, R.J.; Smart, J.E.; Chow, E.

J. Biol. Chem. 261, 4239-4246, 1986

A:Title: Purification and partial sequence analysis of a 37-kDa protein that inhibits F

A:Reference number: A92578; MUID:86140249

A:Accession: A30896

A:Molecule type: protein

A:Residues: 27-50, 54-71, 82-97, 111-123, 'L', 124, 129-134, 'EX', 137-138, 'X', 140, 155-161, 167-1

R:Hyatt, S.L.; Liso, L.; Chapline, C.; Jaken, S.

Biochemistry 33, 1223-1228, 1994

A:Title: Identification and characterization of alpha-protein kinase C binding proteins

A:Reference number: A53507; MUID:94153907

A:Accession: B53507

A:Status: preliminary

A:Molecule type: protein

A:Residues: 59-64, 'T', 66, 82-97 <HYA>

C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip

derlood.

C:Comment: Annexin I has been shown to be both an intracellular and an extracellular pro

teolytic. Unphosphorylated it is a potent inhibitor of the enzyme, mimicking the ameliore

pids. Phosphorylation of annexin I results in loss of its inhibitory activity.

C:Comment: This protein contains four homologous repeats. Each contains an "endoneixin fo

and phospholipid.

C:Genetics:

A:Introns: 22/3; 59/1; 90/3; 128/3; 159/1; 185/3; 204/3; 236/1; 268/1; 287/3; 328/3

C:Superfamily: annexin I; annexin repeat homology

C:Keywords: acetylated amino end; calcium binding; duplication; endoneixin fold; glycop

F:2-346/Product: annexin I status predicted <MAT>

F:45-116/Domain: annexin repeat homology <AX1>

F:56-72/Region: endoneixin fold #status predicted

F:117-188/Domain: endoneixin repeat homology <AX2>

F:128-144/Region: endoneixin repeat homology <AX3>

F:200-272/Domain: endoneixin repeat homology <AX3>

F:212-228/Region: endoneixin repeat homology <AX3>

F:276-346/Domain: annexin repeat homology <AX4>

F:287-303/Region: endoneixin fold #status predicted

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

F:21/Binding site: phosphate (Tyr) (covalent) (by EGF receptor/kinase) #status predicted

F:43/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F:43/Binding site: carbohydrate (Asn) (covalent) (by protein kinase C) #status predicted

F:216/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted

Query Match

100.0%; Score 22; DB 1; Length 346;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMWE 5

DB 2 AMWE 6

RESULT 14

LIMS1

annexin I - mouse

N:Alternate names: calpactin II; lipocortin I; p35; phospholipase A2 inhibitory prote

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1992 #sequence, revision 31-Mar-1992 #text_change 22-Jun-1999

C:Accession: S02181; A39902; A32299

R:Sakata, T.; Iwagami, S.; Tsuruta, Y.; Suzuki, R.; Hojo, K.; Sato, K.; Teraoka, H.

Nucleic Acids Res. 16, 11818, 1988

A:Title: Mouse lipocortin I cDNA.

A:Reference number: S02181; MUID:89098333

A:Accession: S02181

A:Molecule type: mRNA

A:Residues: 1-346 <SAK>

A:Cross-references: EMBL:X07486; NID:952875; PIDN:CAA30371.1; PID:952876

R:Morlick, K.R.; Cheng, I.C.; Wong, W.T.; Wakeland, E.K.; Nick, H.S.

Genomics 10, 365-374, 1991

A:Title: Mouse lipocortin I gene structure and chromosomal assignment; gene duplicati

A:Reference number: A39902; MUID:91301692

A:Accession: A39902

A:Molecule type: DNA

A:Residues: 1-211, 'I', 213-346 <HOR>

A:Cross-references: GB:M69260; NID:9198843; PIDN:AAA39437.1; PID:9198845

A:Note: the authors translated the codon AAT for residue 212 as Arg

R:Phillips, C.; Rose-John, S.; Rincke, G.; Fuertenderger, G.; Marks, F.

Biochem. Biophys. Res. Commun. 159, 155-162, 1989

A:Title: cDNA-cloning, sequencing and expression in glucocorticoid-stimulated quiesce

A:Reference number: A32299; MUID:89165848

A:Accession: A32299

A:Molecule type: mRNA

A:Residues: 6-77, 'P', 80-221, 'H', 223-273, 'H', 275-346 <PHI>

A:Cross-references: GB:M24554; NID:9198761; PIDN:AAA39420.1; PID:9387403

A:Experimental source: Swiss 3T3 cells

C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho

derlood.

C:Comment: Annexin I has been shown to be both an intracellular and an extracellular

activity. Unphosphorylated it is a potent inhibitor of the enzyme, mimicking the ameli

pids. Phosphorylation of annexin I results in loss of its inhibitory activity.

C:Comment: This protein contains four homologous repeats. Each contains an "endoneixin

and phospholipid.

C:Genetics:

A:Gene: Lipol

A:Map position: 19

A:Introns: 22/3; 59/1; 90/3; 128/3; 159/1; 185/3; 204/3; 236/1; 268/1; 287/3; 328/3

C:Superfamily: annexin I; annexin repeat homology

C:Keywords: acetylated amino end; calcium binding; duplication; endoneixin fold; glyco

F:2-346/Product: annexin I status predicted <MAT>

F:45-116/Domain: annexin repeat homology <AX1>

F:56-72/Region: endoneixin fold #status predicted

F:117-188/Domain: endoneixin repeat homology <AX2>

F:128-144/Region: endoneixin repeat homology <AX3>

F:200-272/Domain: endoneixin repeat homology <AX3>

F:212-228/Region: endoneixin repeat homology <AX3>

F:276-346/Domain: annexin repeat homology <AX4>

F:287-303/Region: endoneixin fold #status predicted

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

F:21/Binding site: phosphate (Tyr) (covalent) (by EGF receptor/kinase) #status predic

F:43/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F:43/Binding site: carbohydrate (Asn) (covalent) (by protein kinase C) #status predicted

F:216/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pre

Query Match

100.0%; Score 22; DB 1; Length 346;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
|||||
Db 2 AMVSE 6

RESULT 15

L00P1

annexin I - Rodentia spp.

N:Alternate names: calpactin II; lipocortin I

C:Species: Rodentia spp.

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 01-Aug-1997

C:Accession: S13044; S14429

R:Robitzki, A.; Schroeder, H.C.; Ugarkovic, D.; Gramzow, M.; Fritzsche, U.; Batel, R.; Mu

Biochem. J. 271, 415-420, 1990

A:Title: cDNA structure and expression of calpactin, a peptide involved in Ca(2+)-depend

A:Reference number: S13044; M010:91054405

A:Accession: S13044

A:Molecule type: mRNA

A:Residues: 1-346 <ROB>

A>Note: the authors translated the codon AAA for residue 219 as Leu

A>Note: the source is designated as the sponge Geodia cydonium; the accession EMBL:X1698

R:Mueller, G.
submitted to the EMBL Data Library, October 1989

A:Reference number: S14429

A:Accession: S14429

A:Molecule type: mRNA

A:Residues: 1-113,'T',115-218,'NV',221-222,'T',224-296,'I',298-346 <MUE>

A>Note: the source is designated as the sponge Geodia cydonium; the accession EMBL:X1698

C:Comment: The source of this sequence is now regarded by the author as contamination fr

C:Superfamily: annexin I; annexin repeat homology

C:Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin

F:45-116/Domain: annexin repeat homology <AX1>

F:56-72/Region: endonexin fold #status predicted

F:117-188/Domain: annexin repeat homology <AX2>

F:128-144/Region: endonexin fold #status predicted

F:200-272/Domain: annexin repeat homology <AX3>

F:212-228/Region: endonexin fold #status predicted

F:276-346/Domain: annexin repeat homology <AX4>

F:287-303/Region: endonexin fold #status predicted

F:21/Binding site: phosphate (Tyr) (covalent) #status predicted

F:27/Binding site: phosphate (Ser) (covalent) #status predicted

F:214/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:216/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 22; DB 2; Length 346;

Best Local Similarity 100.0%; Pred No. 92;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
|||||
Db 2 AMVSE 6

Search completed: July 9, 2002, 12:20:15
Job time: 225 sec